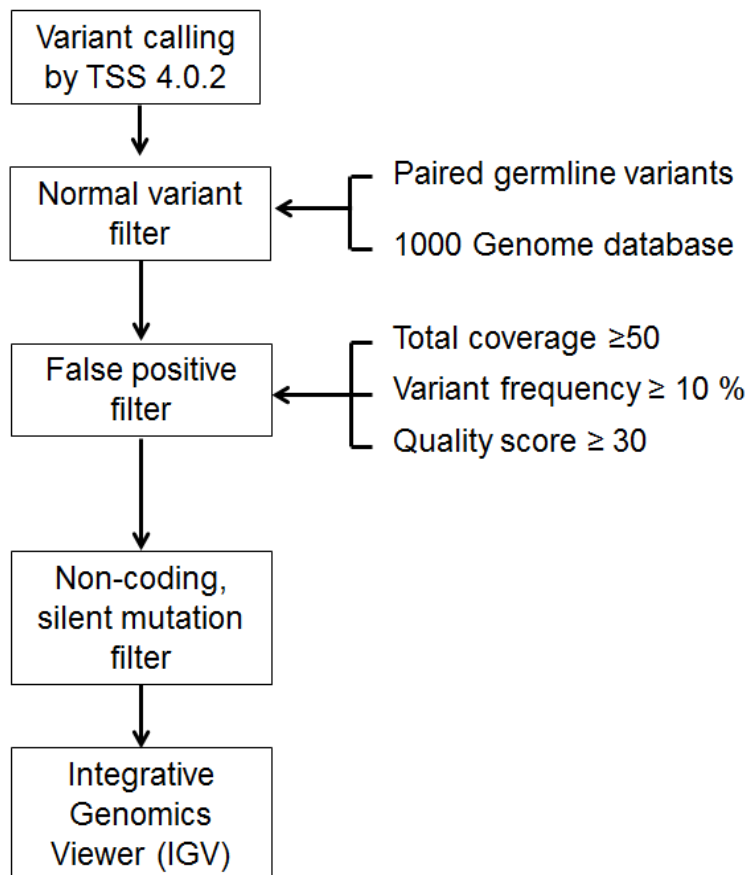
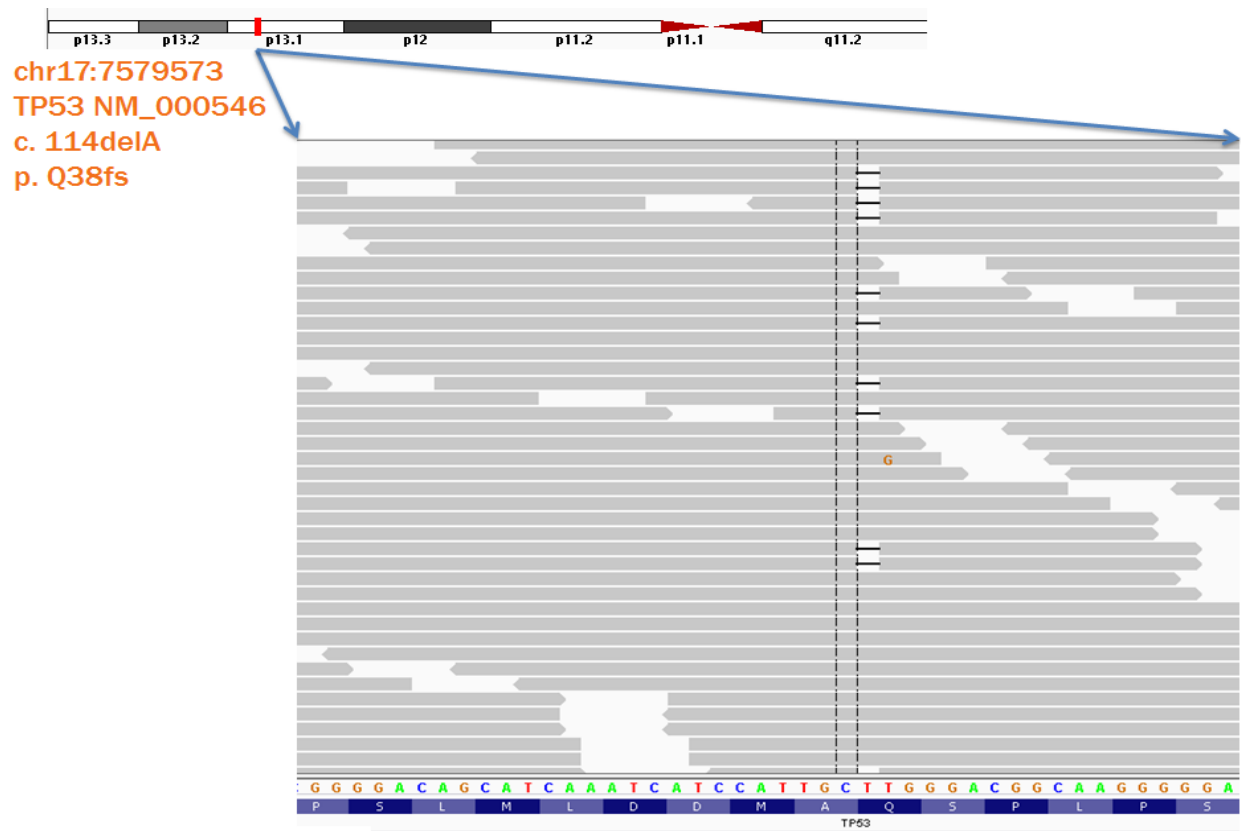


Next-generation sequencing reveals somatic mutations that confer exceptional response to everolimus

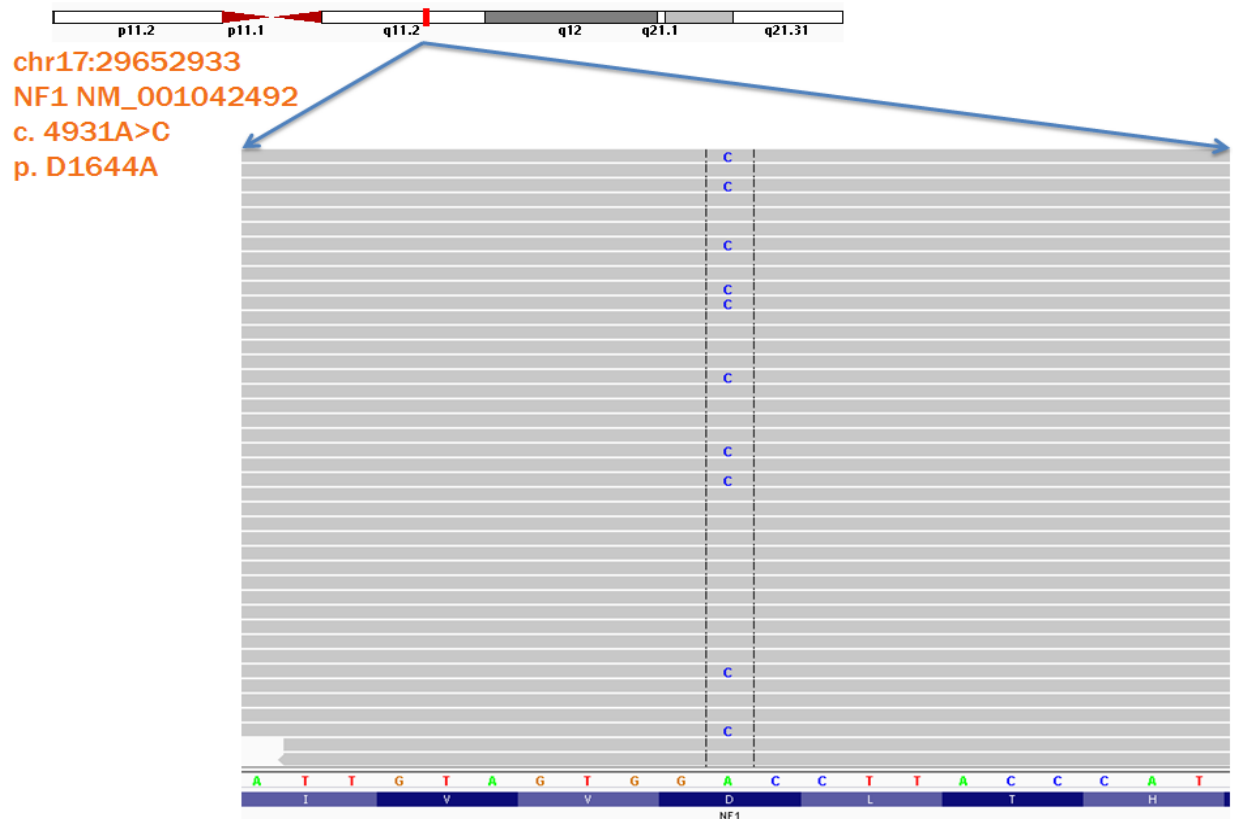
Supplementary Material



Supplementary Fig.S1. Variants acquired from the CCP panel were filtered by germline variants acquired from our patients and 1000 genome data. Mutations with less than 50x depth and less than 10% variant frequency were filtered out. Quality score, a parameter of variant call format (VCF) using phred scale, was used to filter out the variants and Q30 was used for cut-off value. Then, variants were annotated using ANNOVAR and non-coding region and synonymous variants were filtered out.

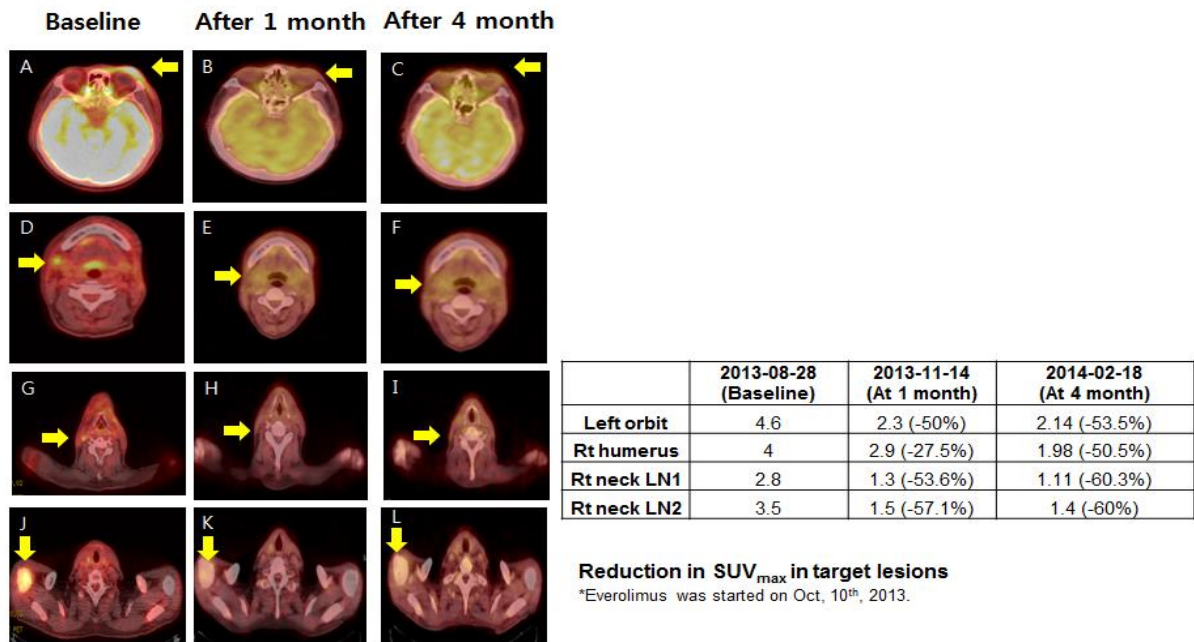


(A) *TP53* (Q38fs) mutation in Integrative Genomics Viewer



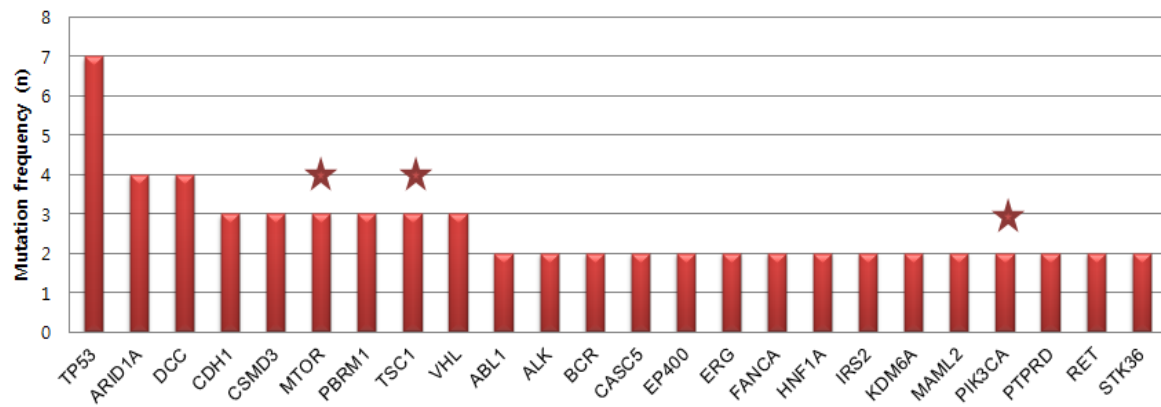
(B). *NF1* (D1644A) mutation in Integrative Genomics Viewer

Supplementary Fig.S2. (A) *TP53* (Q38fs) mutation and (B) *NF1* (D1644A) mutation in Integrative Genomics Viewer

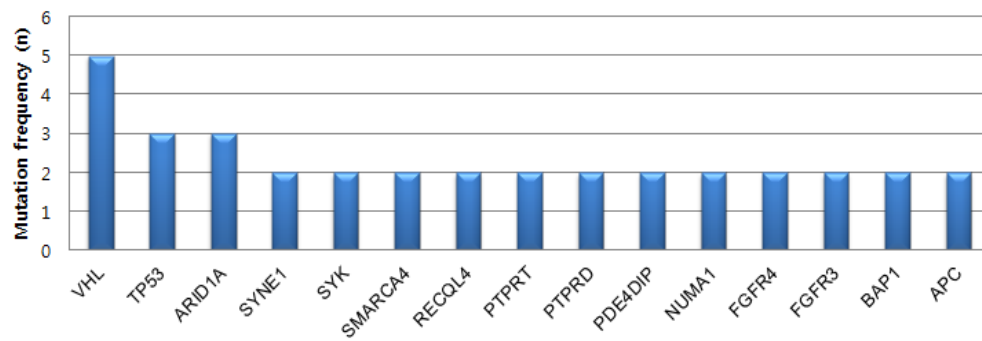


Supplementary Fig.S3. Comparison of PET-CT taken at baseline, after 1 month and after 4 month which showed reduction of SUV_{max} in left orbit (**A, B, C**), right neck nodes (**D, E, F & G, H, I**) and right humerus (**J, K, L**). The patient showed partial response as per PET response criteria.

(A)



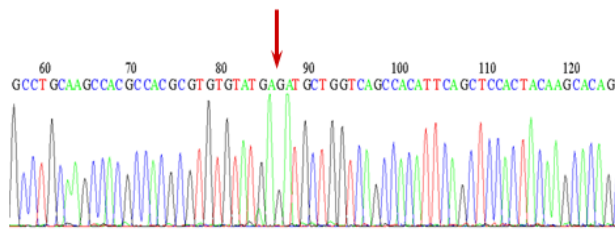
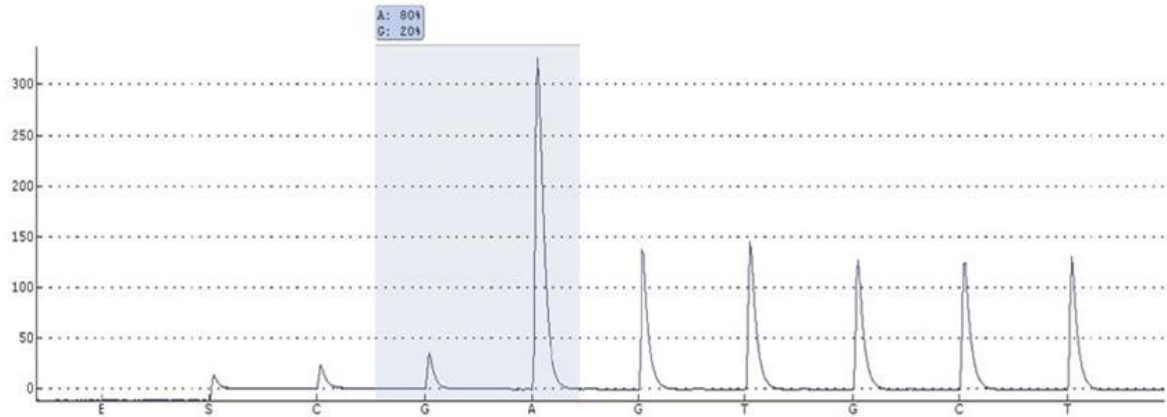
(B)



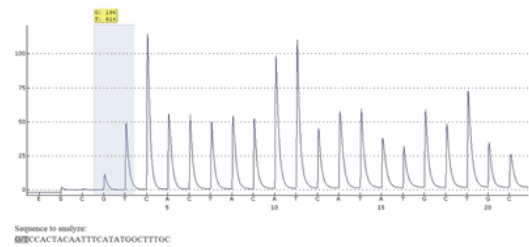
Supplementary Fig.S4. Recurrent genetic alterations seen in patients with **(A)** clinical benefit **(B)** non-clinical benefit

MTOR
p.K1771R (c.5312 A>G)

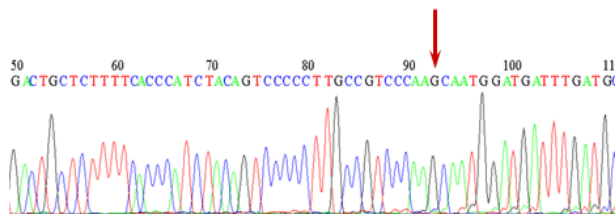
Sequence to analyze: A/GAGTGCTGCA



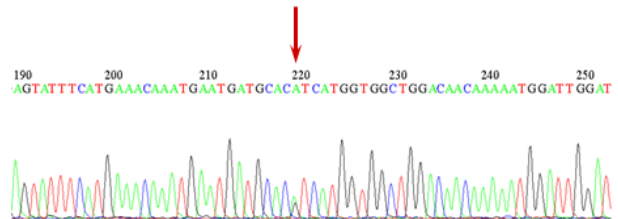
#12 *TSC2*
p.E588K (c.1762 G>A)



#14 *NF1*
p.D1644A (c.4931 A>C)

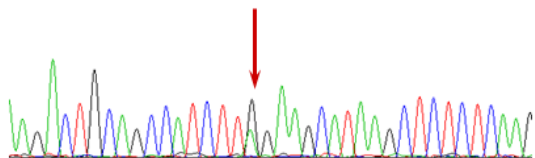


#14 *TP53*
p.Q38fs (c.114 del A)



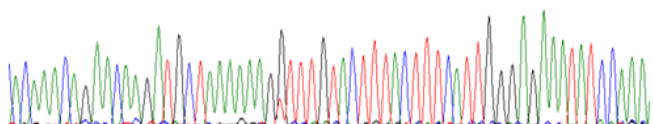
#15 *PIK3CA*
p.H1047R (c.3140 A>G)

...AGACTGCGAGCCTCTTTGGAAAGCATAAAGCTCTCTCTCAAG



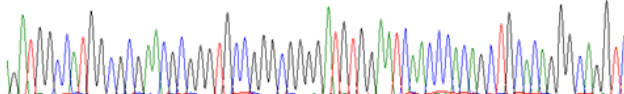
#22 *TSC1*
p.W103X (c.308 G>A)

ACAAACAGAACAGATGCTAAAAAGTTTGTACTTTACTTTTCATTGGAGAAATATCCAAA
70 80 90 100 110 120 130



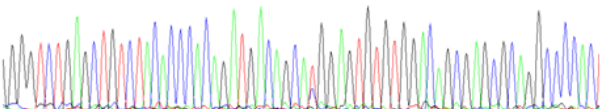
#25 *PTEN*
c.801+1 G>T

GATGGCATTGGCGCGAACCGGGTCCGGGGGGGATGTGGAAATCAACCCACAGCTGCACAGGGCAGGTC
90 100 110 120 130 140 150

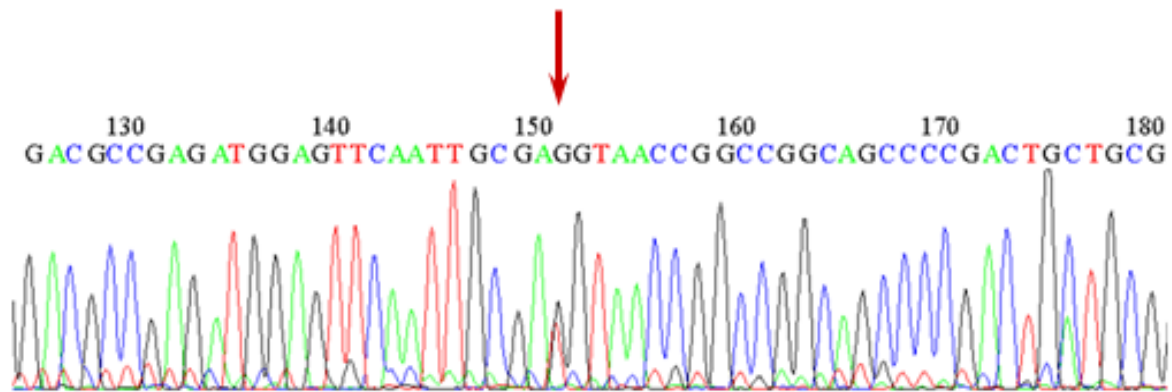


#32 *TP53*
p.P19S (c.55 C>T)

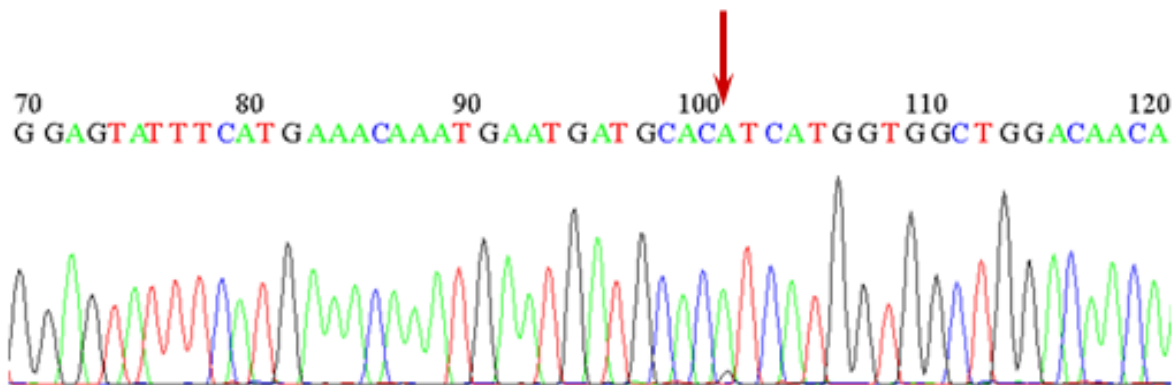
GGGTCTGAGCTGTCTACACCCACAGATGACAGCATGGAGTGTGTGGACAGCGAGCGCAGGCCCCAC
130 140 150 160 170 180 190



#33 *AKT1*
p.M458T (c.1373 T>C)



#38 *NF2*
 p.E38D (c.114 G>T)



#39 *PIK3CA*
 p.H1047R (c.3140 A>G)

Supplementary Fig.S5. Validation of identified mutations in *MTOR*, *TSC1*, *TSC2*, *PIK3CA*, *NF1*, *NF2*, *PTEN*, *AKT1* by Sanger sequencing or pyrosequencing.